

1A

This is Alfin cDNA sequence of the clone as submitted to GenBank #L07291

GAATTCCCTTGACTTTTGTGTTGAAATTGAGGATGGAAGGAATGGCACAGCACCCA
GTACCTCGAACTGTTGAAGAAGTTTTTAGCGATTACAAAGGCAGACGCGCCGGT
TTGATCAAAGCTCTCACTACTGACGTTGAAAAGTTTTACCAGCTCGTCGATCGC
GAAAAGGAGAATTTGTGCCTCTATGGGTTTCCAAATGAAACATGGGAAGTGAAC
TTGCCTGTTGAGGAAGTGCCTCCTGAACTTCCCGAGCCAGCATTGGGTATAAA
CTTTGCTCGGGATGGAATGCAGGAGAAGGACTGGTTATCACTGGTTGCAGTTC
ACAGTGACTCATGGCTGCTCGCTGTTGCTTTCTATTTTGGTGCCCGCTTTGG
ATTTGGTAAGAATGATAGGAAAAGGCTTTTTTCAGATGATAAATGA
TCTGCCCACAGTCTTTGAGCTTGCAACAGGAACTGCTAAGCAATCAAAGGAC
CAACTGACTGCTCACAACAATGGTAGCAATAGCAAATACAAATCAAGTGGAAAGT
CCCGCCAGTCTGAATCCCAGACCAAGGGTGTGAAGATGTCTGCACCGGTCAAAG
AAGAGGTTGACAGTGGAGAAGAAGAGGAAGAAGATGATGATGAACAAGGTGCAAC
CTGTGGTGCTTGTGGTGATAATTATGGCACCGATGAATTCTGGATCTGTTGT
GATATGTGCGAGAAATGGTTCCATGGTAAATGTGTTAAAATTACTCCTGCCAAG
GCTGAACACATCAAGCAATACAAGTGCCCTGGCTGCAGTATCAAGAAGCCAAGAA
TTGGATAGCTCTGAACGTTTGGACCATTAGCGGGCAAGATTAAAATGTTTGTTA
GCATTTCTGTAAGTGAAACCATTTGTTGTCTGCATAGTCACTTAAAGGGAATTCC

FIG. 1A

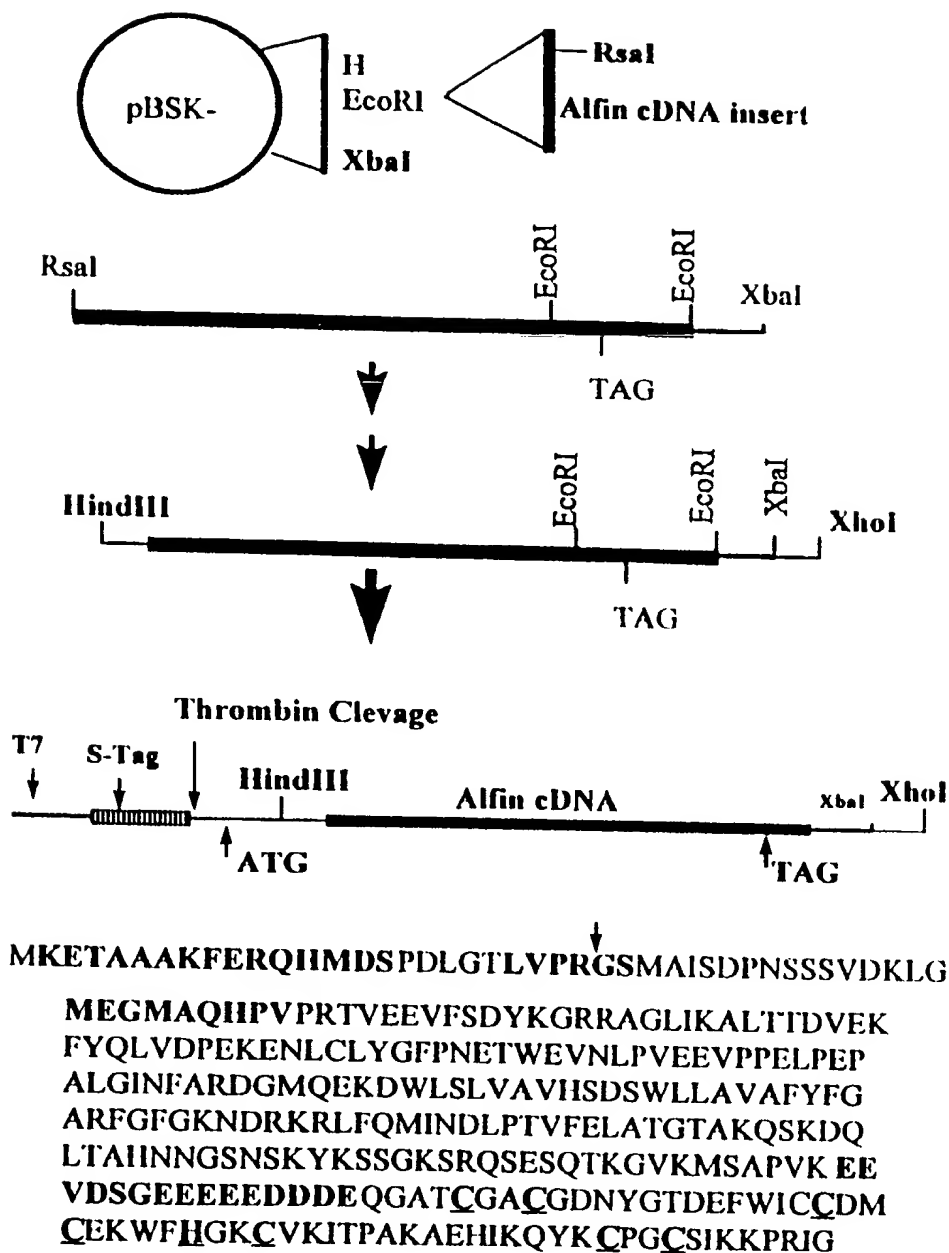


FIG. 1B

DNA Sequences that bind Alfin *in vitro*

<u>Clone</u>	<u>Sequence</u>	
	<u>5'primer</u>	<u>Insert</u>
6	5'GACG-GCTGGGGG	AAAGTGAGCGGTGGCCC 3'
7*	GACG-CAAAGGGGGT	GGGGACGGCGCTTTT
18*	GACG-CAAAGGGGGT	GGGGACGGCGCTTTT
15	GACG-GGTAGGGT	GTGGGGGGTGT TTTTATT
16	GACG-GGGATAGGT	GAGGTGGAGGGACAAT
22	GACG-GCAGAAGGG	GAGAAACGTGGAGAATC
25	GACG-GCGGGAAGG	AGTGTGGTAGAGAGCC
21	GACG-AAGGAAGG	ACGGCAGCGTCTTGC
5	GACG-AAAANTTAN	ANGTGTAGGTGGGACT

* - individual isolates

Consensus: 2-5 Triplets bordered by G and containing at least one GTG, most conforming to the high affinity Zif268 binding sites

MsPRP2 Fragments

211	coding	5' ⁻²⁹⁹ GTGTGGGGCCC ⁻²⁸⁹
	non-coding	5' ⁻³⁹⁰ AAAGTGGGGGCA ⁻³⁹⁸
218	non-coding	5' ⁻⁸²⁶ GATGTGTGTGTTT ⁻⁸³⁸
187	non-coding	5' ⁻⁵⁰⁴ CAAGTGGTGCTG ⁻⁵¹⁵
	non-coding	5' ⁻⁴⁶³ AAAGCGGTGCTG ⁻⁴¹⁴

FIG. 2

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TTTTATAAATATTTAAGCTTGATAATAATTTTGCGATCTATATATAAGCCAC-1501
TACCAATTTAAAATTATATATATATATATATATATATATAATAATTTTTATT-1441
ATATTTATTACGTTGATGGTAAAAAATAAATATAATTTGTTACCATTAAAAAGTCATAA-1381
ATATAGTACAATCCAACCCTTTGAGAGGTTAATGTGTGTGCGGATTTTCTAGATAAAACAA-1321
GGTGCCATTACGATTCTTCTTGGTGCAGCTTGGAGAACCCTATCCTGGGCTTGGAAAGAT-1261
TTACTTCTTGTTGATGCTTCTAGAGTACAGCTCCTTAAGGCTGTAGTCTAGTTTTTTTTTT-1201
TCATCCTTCTACCAAAAAAAAAAAGTCATAAATATAGTTTATACATATAACTTTAATA-1141
AAAATAAAAAAATTTTATCCCTAAAAACATAGTAGAAATTTTATAAAAAAATATTGTTT-1081
ATAATTTACATGCCGTTACCGTAAAAAATGGATAAATTTGGGTATGGAGTACTAGTAATTA-1021
ATAAGGTTCAATTGGTTAAAAAACTAAAAAATAATTTCTCTCCTGATTTATATGAAATGA- 961
CATTTTTTTTGAACATGAAGGGTATTGATTTTTTACCACCTTTTACACCTTTCAAAGCCAT- 901
TCAAGGATGAATATAGATTTTTTGGGCGATCAAACACAAGATCATTACGATAACATGCTT- 841
TGGAAACACACACATGCTTAAATTAATGGTTGGAGTATCAAATTTTAAATATTGTTGTCA- 781
Alfin1*/myc myb*
ATACATACCCCGTCAATCTTCTTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTT- 721
Alfin1*
GTTAAGCATAAAAAACATCAAAGTCTAGCAAAATGTTGTTTTTGGCATGACACATTTTATA- 661
TAGTTTTAAAGGATGCATGATTTCGATTACAAAAACAAAATACTAATAATTCTAGCACAAAG- 601
TfII
TTTAAAGCAAGATTATAAAGCTTCATAGCATGTGGATATTCATTTAGAAATATAGATTAG- 541
myc
ATTGCCCCCTTTCATCACGGGTCTAACAGCACCACCTTGTCACTACATGTCAAAAATGTCTT- 481
myb/Alfin1*/myc
CTAGTACAGCACCGCTTTTTTACTTTGATTCCCCTTGTCCATGCATGAAAAAATCAAAACA- 421
Alfin1* TfII
ATATTTGGACACACAAAACCTTGCCCCACCTTTCCTTTTTTCTTTCTGCCCTAGTTTGTTTGA- 361
Alfin1*
GACTCATATTGATCAAATTTGGCTATGAATTCAAACAAAAAATTCACCTCTACCCATTGCA- 301
myc
TGTGTGGGGCCACATATAAATCCATGAAGGATTTCAATGTCCATCCAAGTCAATGATTG- 241
Alfin1 TfII
AACATATATAACATTGAATAATTTAATTCCAATTTGCAGTATTATGATTTAGATTGATTG- 181
CTGCAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGTATCAAAATTTCAAGGTA- 121
TTTTATTTATTTTTTAACAAATAAAATTTCAAGGTCTTGTTACCATATAAACCTCCTCAG- 61
TCACACCCAATTTCTCTTAAGTGTATGACTTCATAGTACACTACACTACTTTCTTTTGAAC- 1
ATGGCTAACTATGCTCTAGCCAATGTTTTTCATCCTTCTCTTGAACCTTGAGTACCTTACTC- 60
Met

FIG. 3

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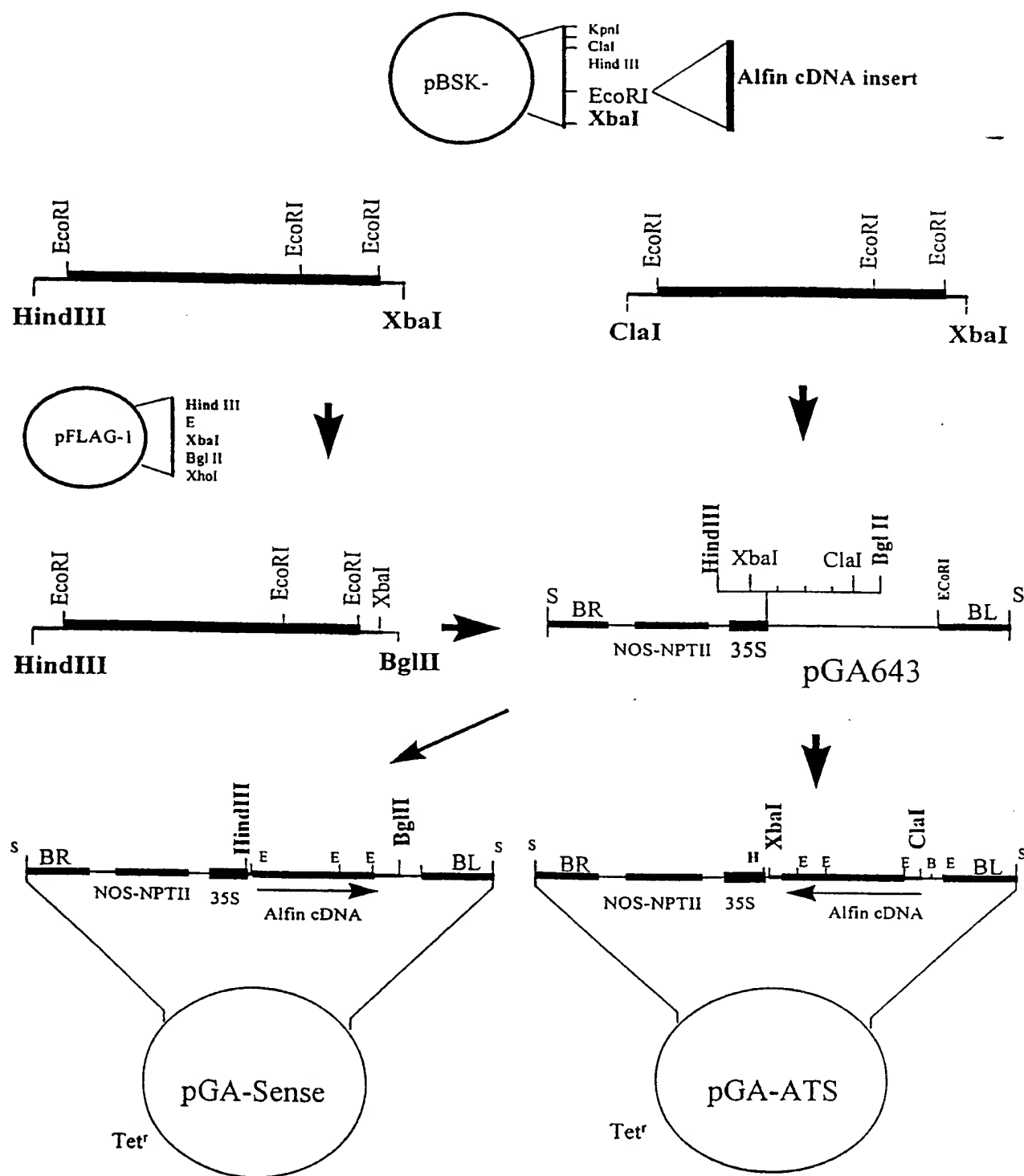
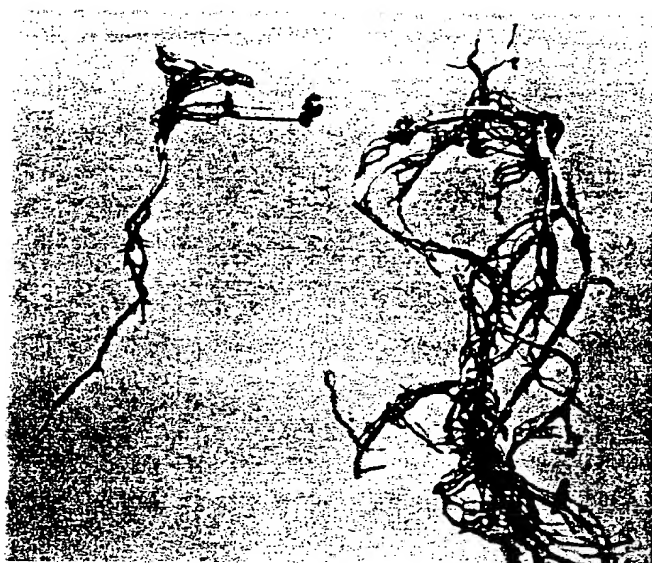


FIG. 4



FIG. 5



A



B

FIG. 5 (continued)

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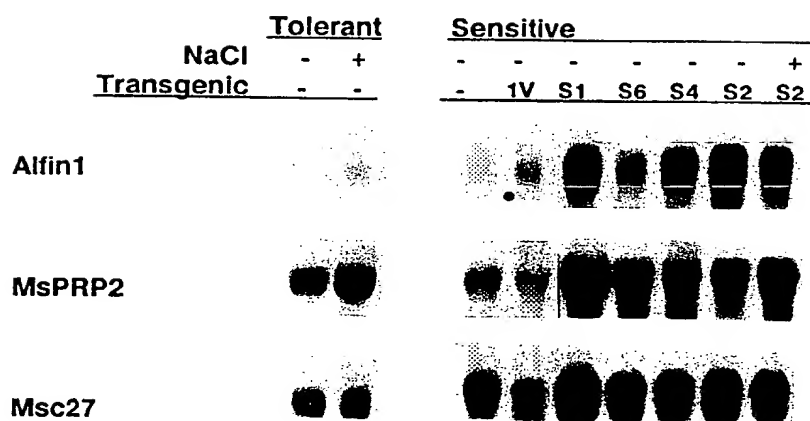


FIG. 6A

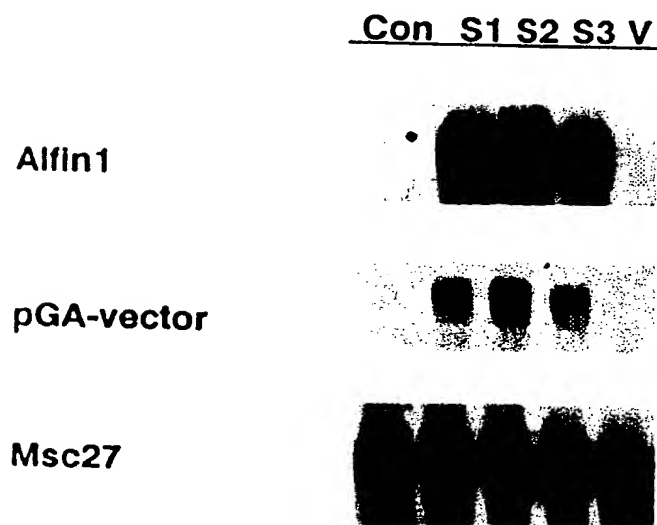


FIG. 6B

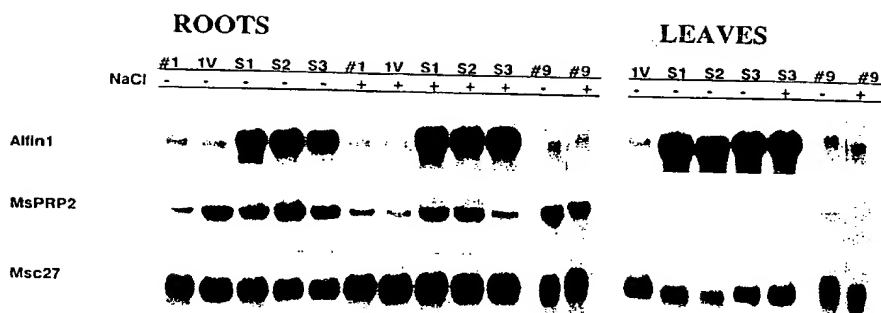


FIG. 6C